

SEQUENCE LISTING

<110> Giese, Klaus
Xin, Hong

<120> METASTATIC BREAST AND COLON CANCER REGULATED GENES

<130> 1451.002 / 210030.447

<140> US 09/215,450

<141> 1998-12-17

<160> 27

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 2429

<212> DNA

<213> human

<400> 1

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aggaagctgg	acgggcttcg	ttggggaaga	cctcgtcacc	atccccaag	gcttcaatac	420
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<210> 2

<211> 486

<212> DNA

<213> human

<220>

<221> misc_feature

<222> (1)...(486)

<223> n = A,T,C or G

<400> 2

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acaatcacgg ctactggag gcctcaattg cctgggctca attaattccc tcattctacc 180
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catttctccc caaatttctg ggattacagg cttaagctac cacacctggc cagccctcaa 360
taatttttaa aattaaaaaa atttctcctaa acccaaaaat ttttaaggacc tktaaggtag 420
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tttttt 486

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<210> 3

<211> 397

<212> DNA

<213> human

<220>

<221> misc_feature

<222> (1)...(397)

<223> n = A,T,C or G

<400> 3

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ttactgtaaa tatgtatata cacatacaaa aaccaggcca ttgttaagag aaaataatgg 120
cccaragggt gaaattatca gacagaacct ttaaaaaata ttatgattaa tgtgttaaaa 180
ttctagtggg aaagataaat aacatgctca ggaaatttta gcagagagat agaaactatg 240
tggaagctc aaatgaaaat gctaggaaat gaaaagcagt attggagggtg aaagattcct 300
ttggcaattt atcaacanac tggagatggc anaggcataa tcagtantat tgaaggcaga 360
ttactatnta ttatncaanc aaaaaaaaaa accccct 397

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<210> 4

<211> 376

<212> DNA

<213> human

<400> 4

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caacagaaac	ttatcttctc	acgggttctga	aggggtggaa	gtccaagatc	gtgggtgtcaa	180
caggcttggg	ttctcccgag	gcctcacccc	ttggcttgca	gacaacagcc	tttttatagc	240
atcctcctac	ggcctttcct	ctgcgcacga	gcactcccag	tgtctgtctc	tctcacctgt	300
tgtagaaca	ccaatcttat	tggatgctat	aggcctccac	ccttatgacg	tcattaaact	360
ttaaatgccg	gttttaa					376

<210> 5

<211> 380

<212> DNA

<213> human

<400> 5

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gtgagcaccg	taacaaaatg	taaatttgcc	attattagga	agtgtctggtg	gcagtgaaga	180
agcaccacag	ccacttgact	cccagtctgg	tgcctctgtc	acaccagaca	acacaggagc	240
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ctgccttctc	ggatactgga	aaggctcgagt	tttctgaact	gcactgattt	tattgcagtt	360
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<210> 6

<211> 2730

<212> DNA

<213> human

<400> 6

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gacacagtc	agtgtgacct	ggacctgtac	aagtccctgc	aggcctggaa	agaccacaag	960
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aagctgtctca	agcgcttgca	gaacaacgac	acgtgcagca	tgccaggcct	cacgtgcttc	1260
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tgcaccagcg ccaacaataa cacgtactgg tgcattgagga ccatcaatga gactcacaat 1380
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taccagctga tgaatgcagt gaacacactg gacagggatg tcctcaacca gctacacgta 1500
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cagccaatga ccagcagttg gtatgaagaa cctttgacat tttgtaaaag gccatttctt 2640
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<210> 7

<211> 218

<212> DNA

<213> human

<220>

<221> misc_feature

<222> (1)...(218)

<223> n = A,T,C or G

<400> 7

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naccgtnatn tetnctnccg tccggtgtcc atnttggccn tcnagacatcc tggtagacg 120
ccgagacaat ataaatgtac aatggatacc cgatgcaaac aatgtattgt ggttaactag 180
gtgtnatccc ncccattgtg ntantaaggg cngntgtc 218

```

<210> 8

<211> 426

<212> DNA

<213> human

<220>

<221> misc_feature

<222> (1)...(426)

<223> n = A,T,C or G

<400> 8

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gtyyatgatc acatctgacg ctatttctat ccccttctc cccgggacct tttcccttc 60
ctccctggga ccttttcccc ttctgttta anaagccagg gctgcctgga ggaagctttg 120

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```

tcagatctag tggaatgtga cctccctgga atatgtgccc aggggtttgt ctaagcagtt 180
tcaggctatg gcctttactc catctggtcc ccacccctct tatctctctc atgtgtggct 240
gcacctggac gcttggacca tagctgtcac agccccctgg ggaggaaccc actccttggc 300
catgtcagcc tgtgcaatgc aaggctcttg tttgatctgt gtgctgacan aaagcccagc 360
ttccttaaga acttttcatg tggaacactt tggttttgag aagaaaataa atcanaaacc 420
attaaa 426

```

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<210> 9
<211> 480
<212> DNA
<213> human

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<220>
<221> misc_feature
<222> (1)...(480)
<223> n = A,T,C or G

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<400> 9
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tgggcnaagc nccnactnag acntntanna nnnccccccg gantanacnt aatgntagnt 180
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gggggcnatt nncataccnt ggaatttaac cccnttctna ctgttcttnt ttgaatnnat 420
tgtntgtnc agtntttgtt caatattgat aagctacgta tttanaaaat atcatgctgt 480

```

```

<210> 10
<211> 402
<212> DNA
<213> human

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<220>
<221> misc_feature
<222> (1)...(402)
<223> n = A,T,C or G

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<400> 10
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agaasagctc ggctctcggc atctgtccac gtgcagggac cacttgggag tgatcatttc 180
aagcaggggt cttggagagc caggctgagg ccaggtcatt ttgggctgtt tgcaatccta 240
actgggtcag ggcgaggcag gccagtgaag ggattaaaac tcttcaccct ctctaggccc 300
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ggggaattcc tggccctgt caaaattctc aggaggctcc aa 402

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<210> 11
<211> 575
<212> DNA
<213> human

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<220>
<221> misc_feature
<222> (1)...(575)

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<223> n = A,T,C or G

<400> 11

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acaacaggct	ggccttgga	cacattcaac	agcacccctga	ggagcccctt	gaaggaacca	180
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tttttctggt	accttactta	cagatgtttt	tggttcctata	ctcttgtaga	agagctgac	300
ccaaaacagt	gggtactgt	atcatcccta	tatgcttggc	agttatttgc	aatcgccacc	360
aggcatttgt	caaggcttct	aatcagatca	gcagactaca	actgattgac	acgtnaaatc	420
agtcaccgtt	ttttccctac	nattacaaaa	ctgccagtcc	tatatggagt	ctgatcacia	480
gactgcagtt	tcttcacaga	tctcaggaag	ttgtcgtggg	gcanaagctt	tttaaaaaca	540
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<210> 12

<211> 442

<212> DNA

<213> human

<400> 12

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gtagccttaa	acaaactac	aaatggccat	actgaatcaa	ataactatat	atataaaaacc	120
ttgggtgtaa	ataagcagac	agaaaatcta	agaatcaac	agactgagaa	tctacttaaa	180
aggcgaagtt	tcccgttatt	tgacaactca	aaagccaact	tagatcctgg	aaatagtaag	240
cattatgtat	atagtacact	taccaggaat	cgagtttagac	aaccagaaaa	gcccawagca	300
akatttgctg	aaawgttcta	aaagcatgcr	caatgtgact	cataacttgg	aggaggatga	360
ggagggaagt	accaagaaga	aactctccaa	gtggcactac	taccaaataca	gtttccattg	420
ctgctttact	tgatgtgaat	aa				442

<210> 13

<211> 332

<212> DNA

<213> human

<220>

<221> misc_feature

<222> (1)...(332)

<223> n = A,T,C or G

<400> 13

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ggagtctgga	aggttttctc	tagagtcttg	gaaagtttct	taagtgggcc	ctggtacaag	180
gtatacgtgt	aagaatgcct	ttattattca	atcagacatt	agggtctaag	aaaaccagg	240
tggggtcata	atgggtttgt	tttcgtatcc	cancggttgt	actcaggcac	cagtttcccc	300
agttctttta	tgtttaactt	ctacatacat	ca			332

<210> 14

<211> 970

<212> DNA

<213> human

<220>

<221> misc_feature

<222> (1)...(970)

<223> n = A,T,C or G

<400> 14

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actctttcac	acccccata	aaagctcagt	atgtaagact	ctatcccaa	gtttgtcgaa	180
gacattgcac	tttgcgaaatg	gaacttcttg	gctgtgaact	gtcgggttgt	tctgagcctc	240
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cttgttccaa	ccaaatgact	ggcatcatta	cacaaggagc	taaagatttt	ggtcatgtac	480
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<210> 15

<211> 528

<212> DNA

<213> human

<220>

<221> misc_feature

<222> (1)...(528)

<223> n = A,T,C or G

<400> 15

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caagatggag	atggctagca	caaaccgatt	ctgttcctct	ttaaagtgtg	tattagccac	120
ttagcaatct	ctatattctt	tcaagtaacc	aagctgttga	ctttcttact	acttgcagta	180
gcctgtcccc	aactttttcca	tccagtgcct	aacctaaaaa	actccttaac	tctgccttga	240
cctgaggaan	accatgctaa	ctggtgttat	tttgtatgta	ccctgtgcct	aattctataa	300
cagtaaacc	catacgcagg	tgggagggag	gaacaccggg	gcctcgggtca	ctctgggggc	360
agtttagatg	ctgtgaaatt	aaacctgttc	taagtgtact	tgtttgaatt	aattgtattg	420
taatattatt	tgttgaatgt	agtaattagg	tatttatgaa	tatattgctg	taattttctga	480
caacatccaa	aaaataaaat	cttcctaata	taaaaaaaaa	aaacccaa		528

<210> 16

<211> 3831

<212> DNA

<213> human

<400> 16

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<211> 518

<212> PRT

<213> human

<400> 19

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Pro Gly Thr Pro Ala Glu Arg His Ala Asp Gly Leu Ala Leu Ala Leu
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Glu Pro Ala Leu Ala Ser Pro Ala Gly Ala Ala Asn Phe Leu Ala Met
 65           70           75           80
Val Asp Asn Leu Gln Gly Asp Ser Gly Arg Gly Tyr Tyr Leu Glu Met
 85           90           95
Leu Ile Gly Thr Pro Pro Gln Lys Leu Gln Ile Leu Val Asp Thr Gly
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Ser Ser Asn Phe Ala Val Ala Gly Thr Pro His Ser Tyr Ile Asp Thr
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Tyr Phe Asp Thr Glu Arg Ser Ser Thr Tyr Arg Ser Lys Gly Phe Asp
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 Ala Cys Lys Thr His Ser Arg Phe Gln Pro Ser Gln Ser Ser Thr Tyr
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 245 250 255
 Gln Ile Ala Leu Asp Asn Ile Gln Val Gly Gly Thr Val Met Phe Cys
 260 265 270
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 275 280 285
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Gly	Ile	Gly	Thr	Pro	Ala	Gln	Asp	Phe	Thr	Val	Val	Phe	Asp	Thr	Gly
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Ser	Ser	Asn	Leu	Trp	Val	Pro	Ser	Val	Tyr	Cys	Ser	Ser	Leu	Ala	Cys
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 325 330 335
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 Leu Pro Thr Glu Ser Gly Glu Leu Trp Ile Leu Gly Asp Val Phe Ile
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 35 40 45
 Asp Pro Ala Trp Lys Tyr Arg Phe Gly Asp Leu Ser Val Thr Tyr Glu
 50 55 60
 Pro Met Ala Tyr Met Asp Ala Ala Tyr Phe Gly Glu Ile Ser Ile Gly
 65 70 75 80
 Thr Pro Pro Gln Asn Phe Leu Val Leu Phe Asp Thr Gly Ser Ser Asn
 85 90 95
 Leu Trp Val Pro Ser Val Tyr Cys Gln Ser Gln Ala Cys Thr Ser His
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 Ser Arg Phe Asn Pro Ser Glu Ser Ser Thr Tyr Ser Thr Asn Gly Gln
 115 120 125
 Thr Phe Ser Leu Gln Tyr Gly Ser Gly Ser Leu Thr Gly Phe Phe Gly
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 Tyr Asp Thr Leu Thr Val Gln Ser Ile Gln Val Pro Asn Gln Glu Phe
 145 150 155 160
 Gly Leu Ser Glu Asn Glu Pro Gly Thr Asn Phe Val Tyr Ala Gln Phe
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 Asp Gly Ile Met Gly Leu Ala Tyr Pro Ala Leu Ser Val Asp Glu Ala
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 Thr Thr Ala Met Gln Gly Met Val Gln Glu Gly Ala Leu Thr Ser Pro
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 Val Val Phe Gly Gly Val Asp Ser Ser Leu Tyr Thr Gly Gln Ile Tyr
 225 230 235 240
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Gln Val Phe Gly Glu Ala Thr Lys Gln Pro Gly Ile Thr Phe Ile Ala		
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Ala Lys Phe Asp Gly Ile Leu Gly Met Ala Tyr Pro Arg Ile Ser Val		
195	200	205
Asn Asn Val Leu Pro Val Phe Asp Asn Leu Met Gln Gln Lys Leu Val		
210	215	220
Asp Gln Asn Ile Phe Ser Phe Tyr Leu Ser Arg Asp Pro Asp Ala Gln		

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Pro	Gly	Gly	Glu	Leu	Met	Leu	Gly	Gly	Thr	Asp	Ser	Lys	Tyr	Tyr	Lys
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			260					265					270		
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Gly	Cys	Glu	Ala	Ile	Val	Asp	Thr	Gly	Thr	Ser	Leu	Met	Val	Gly	Pro
	290					295					300				
Val	Asp	Glu	Val	Arg	Glu	Leu	Gln	Lys	Ala	Ile	Gly	Ala	Val	Pro	Leu
305					310					315					320
Ile	Gln	Gly	Glu	Tyr	Met	Ile	Pro	Cys	Glu	Lys	Val	Ser	Thr	Leu	Pro
				325						330				335	
Ala	Ile	Thr	Leu	Lys	Leu	Gly	Gly	Lys	Gly	Tyr	Lys	Leu	Ser	Pro	Glu
			340					345					350		
Asp	Tyr	Thr	Leu	Lys	Val	Ser	Gln	Ala	Gly	Lys	Thr	Leu	Cys	Leu	Ser
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Gly	Phe	Met	Gly	Met	Asp	Ile	Pro	Pro	Pro	Ser	Gly	Pro	Leu	Trp	Ile
	370					375					380				
Leu	Gly	Asp	Val	Phe	Ile	Gly	Arg	Tyr	Tyr	Thr	Val	Phe	Asp	Arg	Asp
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Ser	Phe	Tyr	Tyr	Asn	Arg	Asp	Ser	Glu	Asn	Ser	Gln	Ser	Leu	Gly	Gly
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				245					250					255	
His	Tyr	Ile	Asn	Leu	Ile	Lys	Thr	Gly	Val	Trp	Gln	Ile	Gln	Met	Lys
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Gly	Val	Ser	Val	Gly	Ser	Ser	Thr	Leu	Leu	Cys	Glu	Asp	Gly	Cys	Leu
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Ala	Leu	Val	Asp	Thr	Gly	Ala	Ser	Tyr	Ile	Ser	Gly	Ser	Thr	Ser	Ser
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Ile	Glu	Lys	Leu	Met	Glu	Ala	Leu	Gly	Ala	Lys	Lys	Arg	Leu	Phe	Asp
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Tyr	Val	Val	Lys	Cys	Asn	Glu	Gly	Pro	Thr	Leu	Pro	Asp	Ile	Ser	Phe
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His	Leu	Gly	Gly	Lys	Glu	Tyr	Thr	Leu	Thr	Ser	Ala	Asp	Tyr	Val	Phe
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Gln	Glu	Ser	Tyr	Ser	Ser	Lys	Lys	Leu	Cys	Thr	Leu	Ala	Ile	His	Ala
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Met	Asp	Ile	Pro	Pro	Pro	Thr	Gly	Pro	Thr	Trp	Ala	Leu	Gly	Ala	Thr
	370					375					380				
Phe	Ile	Arg	Lys	Phe	Tyr	Thr	Glu	Phe	Asp	Arg	Arg	Asn	Asn	Arg	Ile
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